

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/591,576  
Source: IFWP  
Date Processed by STIC: 9/15/06

***ENTERED***



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,576

DATE: 09/15/2006

TIME: 09:13:59

Input Set : A:\SHIMIZU-13111\_sq.txt  
 Output Set: N:\CRF4\09152006\J591576.raw

3 <110> APPLICANT: KAKU, Hanae  
 4 SHIBUYA, Naoto  
 5 MINAMI, Eiichi  
 6 MINAMI, Naoko  
 7 NISHIZAWA, Yoko  
 8 TAKIO, Koji  
 9 DOHMAE, Naoshi  
 11 <120> TITLE OF INVENTION: CHITIN OLIGOSACCHARIDE ELICITOR-BINDING PROTEINS  
 13 <130> FILE REFERENCE: SHIMIZU-13111  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/591,576  
 C--> 15 <141> CURRENT FILING DATE: 2006-08-31  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003451  
 16 <151> PRIOR FILING DATE: 2005-03-02  
 18 <150> PRIOR APPLICATION NUMBER: JP2004-59551  
 19 <151> PRIOR FILING DATE: 2004-03-03  
 21 <160> NUMBER OF SEQ ID NOS: 23  
 23 <170> SOFTWARE: PatentIn version 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1071  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Oryza sativa  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(1071)  
 35 <400> SEQUENCE: 1  
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 37 Met Ala Ser Leu Thr Ala Ala Leu Ala Thr Pro Ala Ala Ala Leu  
 38 1 5 10 15  
 40 ctc ctc ctc gtc ctc ctc gcc gcc ccc gcc tcc gcc gcc aac ttc acc 96  
 41 Leu Leu Leu Val Leu Leu Ala Ala Pro Ala Ser Ala Ala Asn Phe Thr  
 42 20 25 30  
 44 tgc gcg gtg gct tca ggc acc acc tgc aag tcc gcc atc ctc tac acc 144  
 45 Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala Ile Leu Tyr Thr  
 46 35 40 45  
 48 tcc ccc aac gcc acc acc tac ggc aac ctc gtc gcc cgcc ttc aac acc 192  
 49 Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala Arg Phe Asn Thr  
 50 50 55 60  
 52 acc acc ctc ccc gac ctc ctc ggc gcc aac ggc ctc ccc gac ggc acg 240  
 53 Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu Pro Asp Gly Thr  
 54 65 70 75 80  
 56 ctt tcc tcc gcc ccc gtc gcc aat tcc acc gtc aaa atc ccc ttc 288  
 57 Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val Lys Ile Pro Phe  
 58 85 90 95

SLB  
P-6

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Input Set : A:\SHIMIZU-13111\_sq.txt  
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60	cgc tgc cgc tgc aac ggc gac gtc ggc cag tcg gac cgc ctc ccc atc	336
61	Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp Arg Leu Pro Ile	
62	100 105 110	
64	tac gtc gtg cag ccg cag gac ggg ctc gac gcc atc gcg cgc aac gtg	384
65	Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile Ala Arg Asn Val	
66	115 120 125	
68	ttc aac gcc ttc gtc acc tac cag gag atc gcc ggc aac aac atc	432
69	Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala Asn Asn Ile	
70	130 135 140	
72	ccc gac ccc aac aag ata aat gtc agc cag acg ctg tgg att ccg ctg	480
73	Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu Trp Ile Pro Leu	
74	145 150 155 160	
76	ccc tgc agc tgc gac aag gag gaa ggc tct aac gtg atg cac ctc gcc	528
77	Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val Met His Leu Ala	
78	165 170 175	
80	tac agc gtc ggc aaa ggg gag aac acg tcg gcg atc gct gcc aag tac	576
81	Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile Ala Ala Lys Tyr	
82	180 185 190	
84	ggg gtg acg gag tcc acg ctt ctc acc aga aat aag atc gac gac ccc	624
85	Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys Ile Asp Asp Pro	
86	195 200 205	
88	acg aaa ttg cag atg gga cag att cta gat gtc ccg ctc cct gtg tgc	672
89	Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro Leu Pro Val Cys	
90	210 215 220	
92	cgt tca tca atc agc gat acc tca gct gat cac aat ctg atg ctc ctc	720
93	Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn Leu Met Leu Leu	
94	225 230 235 240	
96	ccg gat ggc acc tat gga ttc acc gca gga aac tgc atc cgc tgc agc	768
97	Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys Ile Arg Cys Ser	
98	245 250 255	
100	tgc agt tca act acc tac cag cta aac tgc act gca gta cag aac aag	816
101	Cys Ser Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala Val Gln Asn Lys	
102	260 265 270	
104	gga tgc ccg tca gtg cca ctg tgc aat gga acg ctg aag ctt ggt gag	864
105	Gly Cys Pro Ser Val Pro Leu Cys Asn Gly Thr Leu Lys Leu Gly Glu	
106	275 280 285	
108	acg aac ggc acc ggt tgc gga tca aca acg tgc gcc tac agt ggt tac	912
109	Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala Tyr Ser Gly Tyr	
110	290 295 300	
112	tcc aac agt tca tcg ctc atc ata caa acc agc ctt gca act aat cag	960
113	Ser Asn Ser Ser Leu Ile Ile Gln Thr Ser Leu Ala Thr Asn Gln	
114	305 310 315 320	
116	aca aca gcc tgc cag aga gga gga tct ggg agg tgc cag ttc gct agg	1008
117	Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser Gln Phe Ala Arg	
118	325 330 335	
120	tcc atg tgg agc atg tct gtt atc tcc ttc cac atg gtg ttg atc att	1056
121	Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met Val Leu Ile Ile	
122	340 345 350	
124	atc tgt ttc ctt tga	1071

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Input Set : A:\SHIMIZU-13111\_sq.txt  
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125 Ile Cys Phe Leu
126          355
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 356
131 <212> TYPE: PRT
132 <213> ORGANISM: Oryza sativa
134 <400> SEQUENCE: 2
136 Met Ala Ser Leu Thr Ala Ala Leu Ala Thr Pro Ala Ala Ala Ala Leu
137 1           5           10          15
140 Leu Leu Leu Val Leu Leu Ala Ala Pro Ala Ser Ala Ala Asn Phe Thr
141          20          25          30
144 Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala Ile Leu Tyr Thr
145          35          40          45
148 Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala Arg Phe Asn Thr
149          50          55          60
152 Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu Pro Asp Gly Thr
153 65           70           75          80
156 Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val Lys Ile Pro Phe
157          85          90          95
160 Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp Arg Leu Pro Ile
161          100         105         110
164 Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile Ala Arg Asn Val
165          115         120         125
168 Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala Ala Asn Asn Ile
169          130         135         140
172 Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu Trp Ile Pro Leu
173 145         150         155         160
176 Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val Met His Leu Ala
177          165         170         175
180 Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile Ala Ala Lys Tyr
181          180         185         190
184 Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys Ile Asp Asp Pro
185          195         200         205
188 Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro Leu Pro Val Cys
189          210         215         220
192 Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn Leu Met Leu Leu
193 225         230         235         240
196 Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys Ile Arg Cys Ser
197          245         250         255
200 Cys Ser Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala Val Gln Asn Lys
201          260         265         270
204 Gly Cys Pro Ser Val Pro Leu Cys Asn Gly Thr Leu Lys Leu Gly Glu
205          275         280         285
208 Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala Tyr Ser Gly Tyr
209          290         295         300
212 Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu Ala Thr Asn Gln
213 305         310         315         320
216 Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser Gln Phe Ala Arg
217          325         330         335

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220 Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met Val Leu Ile Ile
221          340           345           350
224 Ile Cys Phe Leu
225          355
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 987
230 <212> TYPE: DNA
231 <213> ORGANISM: Oryza sativa
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (1)..(987)
238 <400> SEQUENCE: 3
239 gcc aac ttc acc tgc gcg gtg gct tca ggc acc acc tgc aag tcc gcc      48
240 Ala Asn Phe Thr Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala
241 1          5           10           15
243 atc ctc tac acc tcc ccc aac gcc acc acc tac ggc aac ctc gtc gcc      96
244 Ile Leu Tyr Thr Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala
245 20          25           30
247 cgc ttc aac acc acc ctc ccc gac ctc ctc ggc gcc aac ggc ctc      144
248 Arg Phe Asn Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu
249 35          40           45
251 ccc gac ggc acg ctt tcc tcc gcc ccc gtc gcc gcc aat tcc acc gtc      192
252 Pro Asp Gly Thr Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val
253 50          55           60
255 aaa atc ccc ttc cgc tgc cgc tgc aac ggc gac gtc ggc cag tcg gac      240
256 Lys Ile Pro Phe Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp
257 65          70           75           80
259 cgc ctc ccc atc tac gtc gtg cag ccg cag gac ggg ctc gac gcc atc      288
260 Arg Leu Pro Ile Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile
261 85          90           95
263 gcg cgc aac gtg ttc aac gcc ttc gtc acc tac cag gag atc gcc gcc      336
264 Ala Arg Asn Val Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala
265 100         105          110
267 gcg aac aac atc ccc gac ccc aac aag ata aat gtc agc cag acg ctg      384
268 Ala Asn Asn Ile Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu
269 115         120          125
271 tgg att ccg ctg ccc tgc agc tgc gac aag gag gaa ggc tct aac gtg      432
272 Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val
273 130         135          140
275 atg cac ctc gcc tac agc gtc ggc aaa ggg gag aac acg tcg gcg atc      480
276 Met His Leu Ala Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile
277 145         150          155           160
279 gct gcc aag tac ggg gtg acg gag tcc acg ctt ctc acc aga aat aag      528
280 Ala Ala Lys Tyr Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys
281 165         170          175
283 atc gac gac ccc acg aaa ttg cag atg gga cag att cta gat gtc ccg      576
284 Ile Asp Asp Pro Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro
285 180         185          190
287 ctc cct gtg tgc cgt tca tca atc agc gat acc tca gct gat cac aat      624

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288	Leu Pro Val Cys Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn			
289	195	200	205	
291	ctg atg ctc ctc ccg gat ggc acc tat gga ttc acc gca gga aac tgc	672		
292	Leu Met Leu Leu Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys			
293	210	215	220	
295	atc cgc tgc agc tgc agt tca act acc tac cag cta aac tgc act gca	720		
296	Ile Arg Cys Ser Cys Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala			
297	225	230	235	240
299	gta cag aac aag gga tgc ccg tca gtg cca ctg tgc aat gga acg ctg	768		
300	Val Gln Asn Lys Gly Cys Pro Ser Val Pro Leu Cys Asn Gly Thr Leu			
301	245	250	255	
303	aag ctt ggt gag acg aac ggc acc ggt tgc gga tca aca acg tgc gcc	816		
304	Lys Leu Gly Glu Thr Asn Gly Thr Gly Cys Gly Ser Thr Cys Ala			
305	260	265	270	
307	tac agt ggt tac tcc aac agt tca tcg ctc atc ata caa acc acc agc ctt	864		
308	Tyr Ser Gly Tyr Ser Asn Ser Ser Leu Ile Ile Gln Thr Ser Leu			
309	275	280	285	
311	gca act aat cag aca aca gcc tgc cag aga gga gga tct ggg agg tcg	912		
312	Ala Thr Asn Gln Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser			
313	290	295	300	
315	cag ttc gct agg tcc atg tgg agc atg tct gtt atc tcc ttc cac atg	960		
316	Gln Phe Ala Arg Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met			
317	305	310	315	320
319	gtg ttg atc att atc tgt ttc ctt tga	987		
320	Val Leu Ile Ile Ile Cys Phe Leu			
321	325			
324	<210> SEQ ID NO: 4			
325	<211> LENGTH: 328			
326	<212> TYPE: PRT			
327	<213> ORGANISM: Oryza sativa			
329	<400> SEQUENCE: 4			
331	Ala Asn Phe Thr Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala			
332	1	5	10	15
335	Ile Leu Tyr Thr Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala			
336	20	25	30	
339	Arg Phe Asn Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu			
340	35	40	45	
343	Pro Asp Gly Thr Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val			
344	50	55	60	
347	Lys Ile Pro Phe Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp			
348	65	70	75	80
351	Arg Leu Pro Ile Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile			
352	85	90	95	
355	Ala Arg Asn Val Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala			
356	100	105	110	
359	Ala Asn Asn Ile Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu			
360	115	120	125	
363	Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val			
364	130	135	140	

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 09/15/2006  
PATENT APPLICATION: US/10/591,576                    TIME: 09:14:00

Input Set : A:\SHIMIZU-13111\_sq.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 2,5,13,30

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,14,15,16,17,18,19,20,21,22,23

**VERIFICATION SUMMARY**

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Input Set : A:\SHIMIZU-13111\_sq.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

M:341 Repeated in SeqNo=9